

FIGURE 1-1

FIGURE 1-1
FIGURE 1-2
FIGURE 1-3
FIGURE 1-4
FIGURE 1-5

-80 -60 -40
-28 AGTATTGTTGTCGTGTTGCCCTTGTTAGGGCGTCATCCCTCAAGTGATCACTAGTTCAA 31

-20 -1 20
32 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 91
-8 M N T S H L L A L L L

40 60 80
92 CCAAAATCTCCACAAGGTGAAAACAGAAAGCAACCCCTGGGCAACCCATACAACTTCTCT 151
12 P K S P Q G E N R S K P L G T P Y N F S 31

100 120 140
152 GAACATTGCCAGGATTCCGTTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 211
32 E H C Q D S V D V M V F I V T S Y S I E 51

160 180 200
212 ACTGTCGTGGGGTCCCTGGGTAACCTCTGCCTGATGTGTGTAAGTGTGAGGCAAGGAG 271
52 T V V G V L G N L C L M C V T V R Q K E 71

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FIGURE 1-2

220 240 260 331
 272 AAAGCCAACGTGACCAACCTGCTTATCGCCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 91
 72 K A N V T N L L I A N L A F S D F L M C

280 300 320 391
 332 CTCCTCTGCCAGCCGCTGACCGCCGCTACACCATCATGGACTACTGGATCTTTGGAGAG 111
 92 L L C Q P L T A V Y T I M D Y W I F G E

340 360 380 451
 392 ACCCTCTGCAAGATGTGGCCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 131
 112 T L C K M S A F I Q C M S V T V S I L S

400 420 440 511
 452 CTCGTCCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCCAACAGGCTGGAAGCCC 151
 132 L V L V A L E R H Q L I I N P T G W K P

460 480 500 571
 512 AGCATCTCACAGGCCCTACCTGGGGATTGTGCTCATCTGGGTGCTGCTGCTCTCTCC 171
 152 S I S Q A Y L G I V L I W V I A C V L S

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FIGURE 1-3

572	CTGCCCTTCCTGGCCAAACAGCATCCTCGAGAAATGCTCTCCACAAGAACCACTCCAAGGCT	540	560	631
172	L P F L A N S I L E N V F H K N H S K A			191
	580	600	620	
632	CTGGAGTTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCCTGGCCACTGGCTCACCAACCGC			691
192	L E F L A D K V V C T E S W P L A H H R			211
	640	660	680	
692	ACCATCTACACCACCTTCCTGCTCTCTCCAGTACTGCCCTCCCACTGGGCTTCATCCTG			751
212	T I Y T T F L L L F Q Y C L P L G F I L			231
	700	720	740	
752	GTCTGTTATGCACGCACTACCGGCGCCTGCAGAGGCAGGGCGCTGTTTCACAAGGGC			811
232	V C Y A R I Y R R L Q R Q G R V F H K G			251
	760	780	800	
812	ACCTACAGCTTGGGAGCTGGGCACATGAAGCAGGTCAATGTGGTGTGGTGGTGATGGTG			871
252	T Y S L R A G H M K Q V N V V L V V M V			271

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FIGURE 1-4

872	GTGGCCTTTGCCCTGCTCTGGCTGCCTCTGTCATGTGTTCAACAGCCTGGAAGACTGGCAC	931
272	V A F A V L W L P L H V F N S L E D W H	291
	820 840 860	
	880 900 920	
932	CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACCTTGCTTCCC	991
292	H E A I P I C H G N L I F L V C H L L A	311
	940 960 980	
992	ATGGCCTCCACCTGCGTCAACCCATCTCATCTATGGCTTCTCAACACCACTTCAAGAAG	1051
312	M A S T C V N P F I Y G F L N T N F K K	331
	1000 1020 1040	
1052	GAGATCAAGGCCCTGGTGTGACTTGCCAGCAGAGCGCCCCCTGGAGGAGTCGGAGCAT	1111
332	E I K A L V L T C Q Q S A P L E S E H	351
	1060 1080 1100	
1112	CTGCCCCCTGCCACAGTACATACGGAAGTCTCCAAGGTCCCTGAGGCTAAGTGGCAGG	1171
352	L P L S T V H T E V S K G S L R L S G R	371

FIGURE 1-5

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1172	TCCAATCCCA	1120	1140	1160	1231
372	TTTAACCA				375
	GGTCTAGG				
	TCTCTCC				
	CTGTC				
	CCATG				
	TCC				
	CTTGC				
	AGCTTC				
	CTG				
	1180	1200	1220		
1232	CACTAGCTA				1291
	AGTGGG				
	CACACTG				
	CAAGCTG				
	GGGTGG				
	CACCC				
	CAGCAT				
	TCC				
	TGG				
	CTT				
	CTC				
	TG				

FIGURE 2-1
FIGURE 2-2
FIGURE 2-3

FIGURE 2-1

1	50
hp25a	MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQSDVDV MVFIVTSYSI
human Y1	MN.STLFSQV ENHSHVSHNFS ERNAQLLAFE NDDCHLPLAM IFTLALAYGA
rat Y1	MN.STLFSRV ENYSHVHYNVS E.NSPFLAFE NDDCHLPLAV IFTLALAYGA
mouse Y1	MN.STLFSKV ENHSHIYNAS E.NSPLLAFE NDDCHLPLAV IFTLALAYGA
51	100
hp25a	ETVVGVLGNI CLMCVTVRQK EKANVTNLI ANIAPSDFIM CLLCQPLTAY
human Y1	VIILGVSGNI ALIIIIILKQK EMRNVTNILI VNISPSDLLV AIMCLPFFTV
rat Y1	VIILGVSGNI ALIIIIILKQK EMRNVTNILI VNISPSDLLV AVMCLEPFFTV
mouse Y1	VIILGVSGNI ALIIIIILKQK EMRNVTNILI VNISPSDLLV AVMCLEPFFTV
101	150
hp25a	YTINDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGNK
human Y1	YTLMDHNVFG EAMGKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR
rat Y1	YTLMDHNVFG ETMCKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR
mouse Y1	YTLMDHNVFG ETMCKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR
151	200
hp25a	PSISQAYIGI VLIWIA CVL SLIPFIANSIN ENVFHKNHSHK ALEFLADKVV
human Y1	PNNRHAYVGI AVIWI LAVAS SLIPFIYQVM TDEPFQNVV. LDAYKDKYV
rat Y1	PNNRHAYVGI TVIWI LAVAS SLIPFIYQIL TDEPFQNVV. LAAFKDKYV
mouse Y1	PNNRHAYVGI TVIWI LAVAS SLIPFIYQIL TDEPFQNVV. LAAFKDKYV

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FIGURE 2-2

hp25a	201	CTESWPLAHH	RTIYTFLL	FQYCLPLGFI	LVQYARIYRR	LQYGRVFFHK	250
human Y1		CFDQFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
rat Y1		CFDKFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
mouse Y1		CFDKFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
			V				
	251	GTYS.LRAGH	MKQNVVLLV	MVAFAVLMH	PLHVFNSLED	WNHQAIPICH	300
hp25a		MRDNKYRSSE	TKRINIMLLS	IVVAFVVCWL	PLTI FNTVFD	WNHQA IATCN	
human Y1		IRDSKYRSSE	TKRINVMLLS	IVVAFVVCWL	PLTI FNTVFD	WNHQA IATCN	
rat Y1		IRDSKYRSSE	TKRINIMLLS	IVVAFVVCWL	PLTI FNTVFD	WNHQA IATCN	
mouse Y1			VI				
	301	GNLITLVCHL	LAMASTCVNP	FVYGPLNTNF	KKEIKALVLT	CQQSAPLEES	350
hp25a		HNLLFLLCHE	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
human Y1		HNLLFLLCHE	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
rat Y1		HNLLFLLCHE	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
mouse Y1		HNLLFLLCHE	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
			VII				

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FIGURE 2-3

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hp25a	351	388
human Y1	PHLPSTVHT EVSKGSRRLS GRSNPI*....
rat Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKINN	NDDNEKI*
mouse Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM	N.DNEKI*
	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM	N.DNEKV*

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FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

-170

-150

-130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110

-90

-70

TTCTTACCTGGTTCATTTTACATGCCTGGACCTTTGAGTTCCATTGTGTTGTTTGCAG

-50

-30

-10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG

M

10

30

50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCTTACAAGGTAAGAATGGGACC

N T S H L M A S L S P A F L Q G K N G T

70

90

110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCGGCAGATCTGTTG

N P L D S L Y N L S D G C Q D S A D L L

130

150

170

GCCTTCATCATCACCACTACAGCGTTGAGACCGTCTTGGGGGTCCTAGGAAACCTCTGC

A F I I T T Y S V E T V L G V L G N L C

190

210

230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC

L I F V T T R Q K E K S N V T N L L I A

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FIGURE 3-2

250 270 290
AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC
N L A F S D F L M C L I C Q P L T V T Y

310 330 350
ACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAAGATGTTAACGTTTCATCCAG
T I M D Y W I F G E V L C K M L T F I Q

370 390 410
TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCTGGAGAGGCACCAG
C M S V T V S I L S L V L V A L E R H Q

430 450 470
CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCTCCAGGCCTACCTGGGGATTGTG
L I I N P T G W K P S I S Q A Y L G I V

490 510 530
GTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCTGGCCAATAGCATCCTGAAC
V I W F I S C F L S L P F L A N S I L N

550 570 590
GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCTGGAAGACAAGGTTGTCTGC
D L F H Y N H S K V V E F L E D K V V C

610 630 650
TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC
F V S W S S D H H R L I Y T T F L L L F

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FIGURE 3-3

670 690 710
CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG
Q Y C V P L A F I L V C Y M R I Y Q R L

730 750 770
CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG
Q R Q R R A F H T H T C S S R V G Q M K

790 810 830
CGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGCAGTTCTCTGGCTGCCCCCTG
R I N G M L M A M V T A F A V L W L P L

850 870 890
CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC
H V F N T L E D W Y Q E A I P A C H G N

910 930 950
CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTCATC
L I F L M C H L F A M A S T C V N P F I

970 990 1010
TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT
Y G F L N I N F K K D I K A L V L T C R

1030 1050 1070
TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC
C R P P Q G E P E P L P L S T V H T D L

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FIGURE 3-4

1090 1110 1130
TCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCATGTAGTCATGTCTAGGCTCT
S K G S M R M G S K S N V M *

1150 1170 1190
TCCGCCATTTTCTTTGACACACCCTTTCACTGAGCTAAGTAGACACAATGCAAGCTGTG

1210 1230 1250
GTATCATCCTGCCATTTCTGGTCTTTGGGGCCAGACAGGCGGCAAGAGACTTGAAGCTT

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FIGURE 4

1 50

Y4rat MNTSHLMASL SPAFLQKNG TNPLDSLNL SDGCQDSADL LAFIITTSV
Y4hum MNTSHLLALL LPKSPQGENR SKPLGTFYNF SEHCQDSVDV MVFIVTSYSI

51 100

— I — II —

Y4rat ETVLGVLGNL CLIFVTTRQK ERSNVTNLLI ANLAFSDFLM CLICQPLTVT
Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLICQPLTAV

101 150

— III —

Y4rat YTIMDYWIFG EVLCRMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK
Y4hum YTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK

151 200

— IV —

Y4rat PSISQAYLGI VVINFI SCFL SLPFLANSIL NDLFHYNHSK VVEFLEDKVV
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKNHSK ALEFLADKVV

201 250

— V —

Y4rat CFVSNSSDHH RLIYTTFLLL PQYCVPLAFI LVCYMRIYQR LQRORRAFHT
Y4hum CTESWPLAHH RTIYTTFLLL PQYCLPLGFI LVCYARIYRR LQRQGRVPHK

251 300

— VI —

Y4rat HTCSSRVGQM KRINGMLMAN VTAPAVLWLP LHVFNTELEDW YQRAIPACHG
Y4hum GTYSLRAGHM KQVNVVLVVM VVAPAVLWLP LHVFNTELEDW HHEAIPICHG

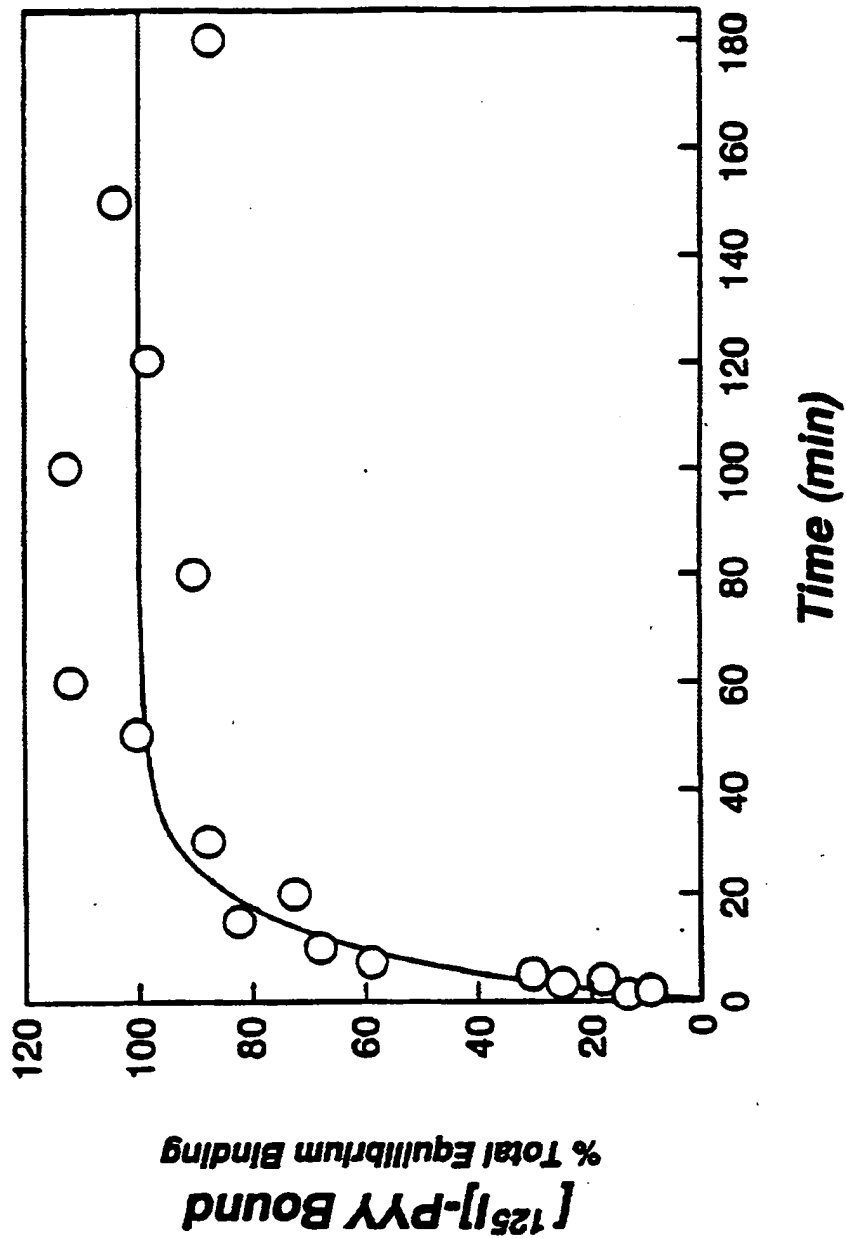
301 350

— VII —

Y4rat NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTG RCRPPQGEPE
Y4hum NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KBIKALVLTG QQSAPLEESE

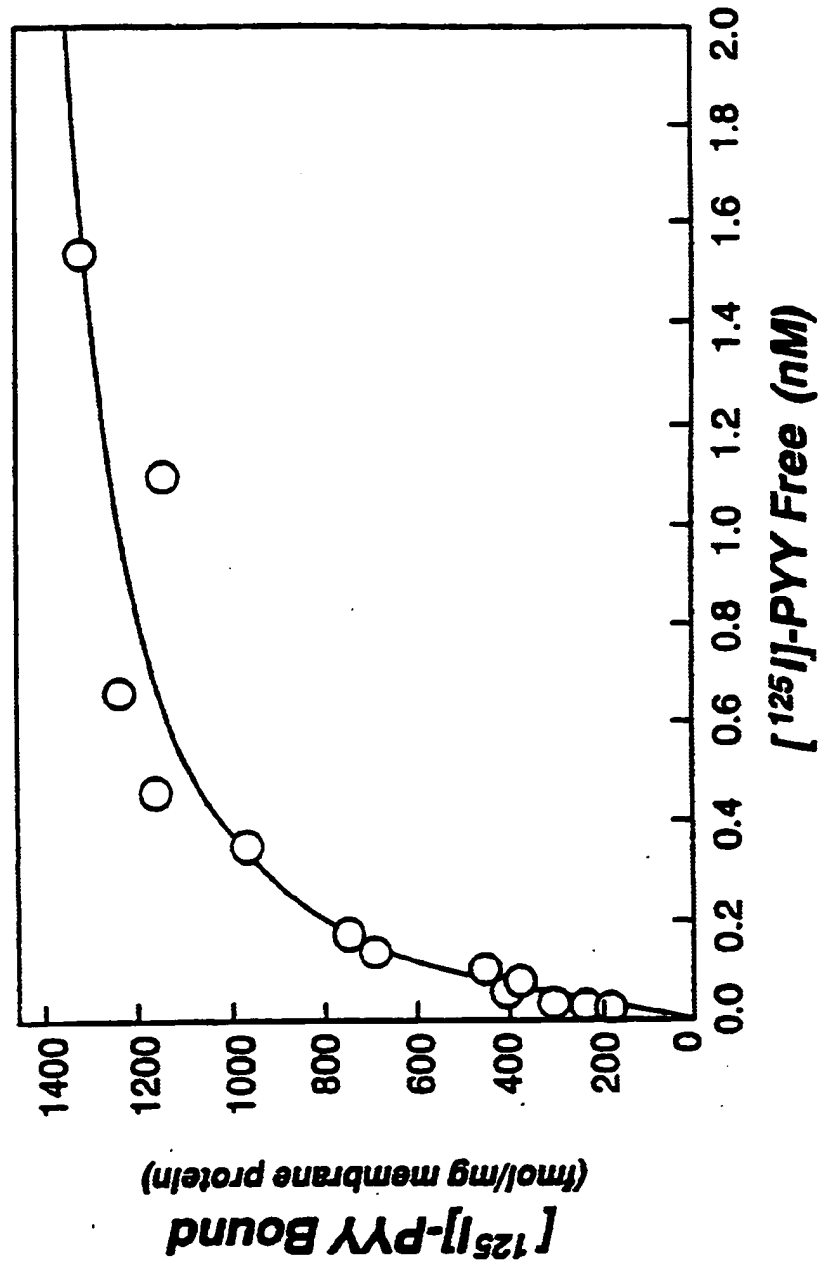
25ETFO* 35956480

FIGURE 5



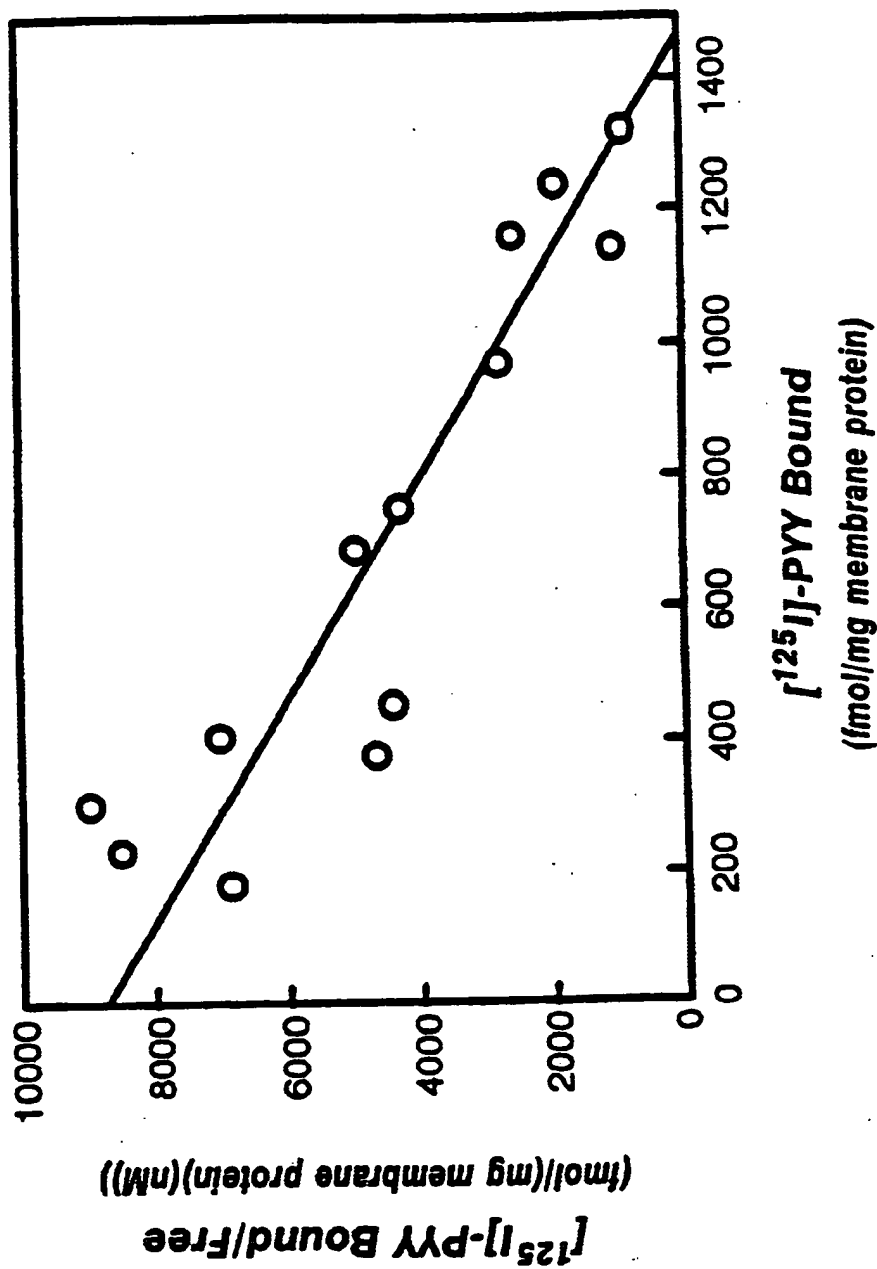
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FIGURE 6A



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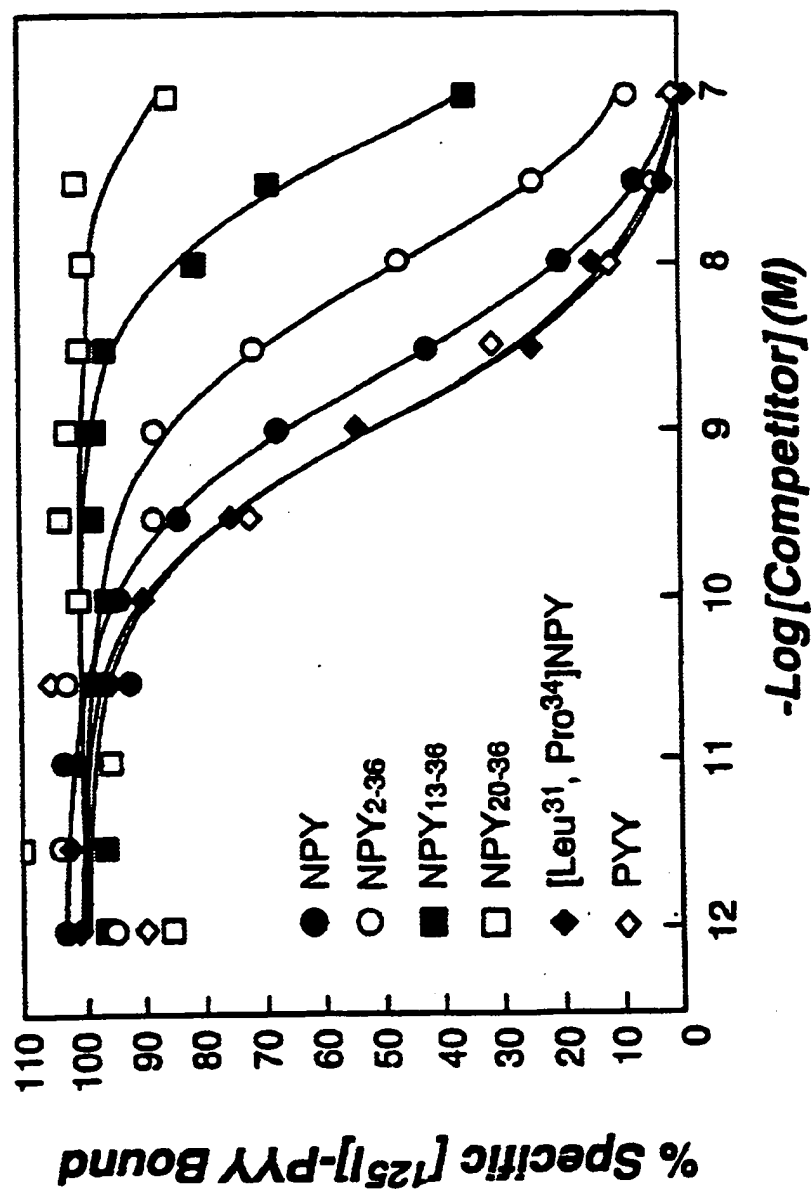
FIGURE 6B



26EFD* 56956480

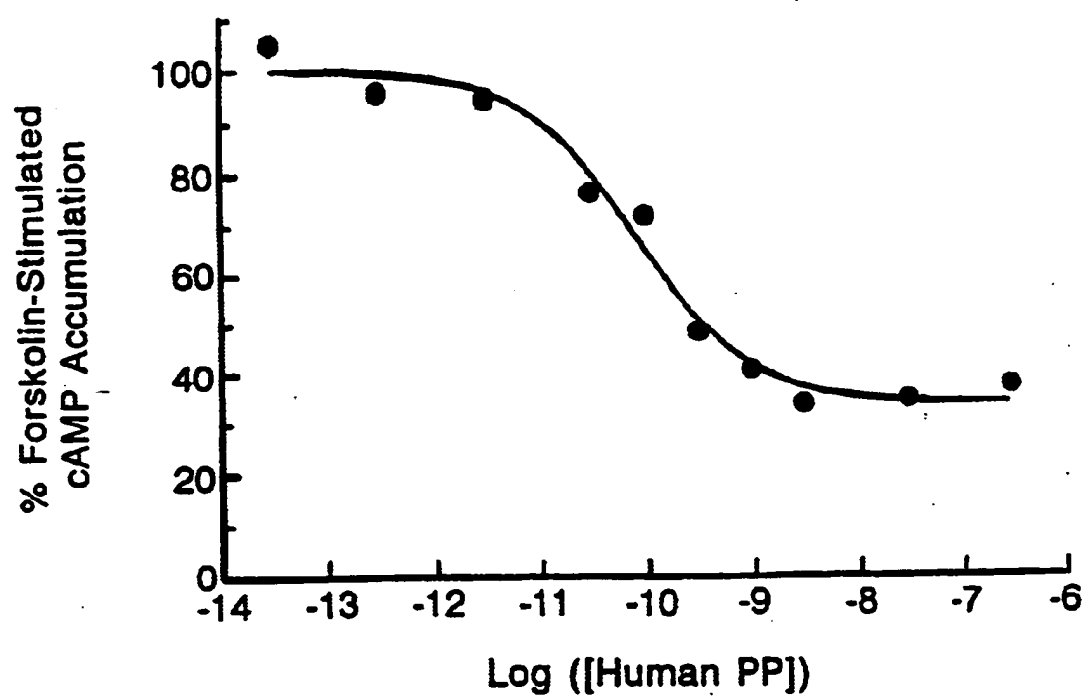
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FIGURE 7

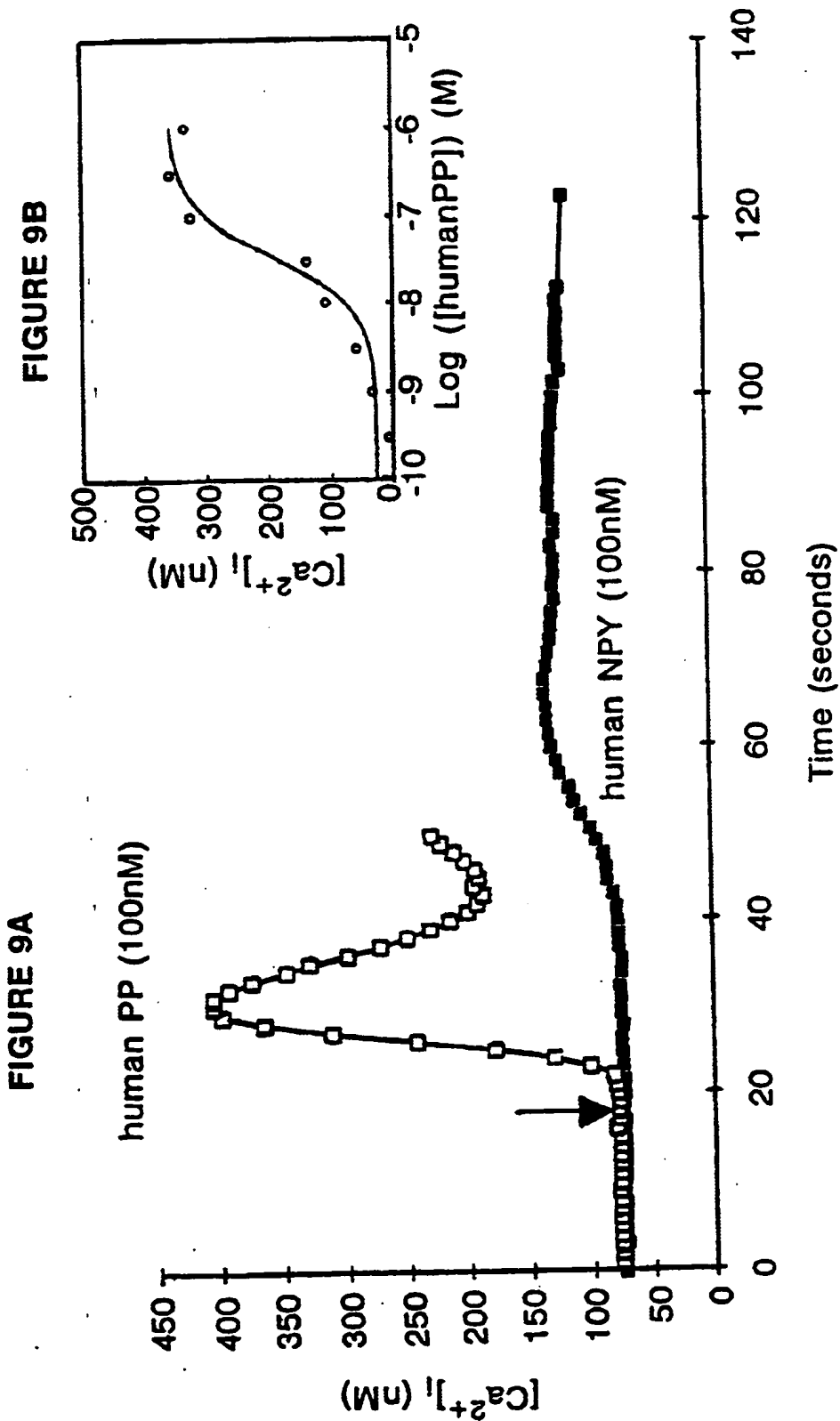


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FIGURE 8



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